#2

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/086,156

DATE: 03/19/2002 P.5
TIME: 16:22:30

Input Set : A:\EP.txt
Output Set: N:\CRF3\03192002\J086156.raw

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   3 <110> APPLICANT: Bristol-Myers Squibb Company
   5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNITS,
   6        K+betaM4 and K+betaM5
   8 <130> FILE REFERENCE: D0115NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/086,156
C--> 10 <141> CURRENT FILING DATE: 2002-02-28
  10 <150> PRIOR APPLICATION NUMBER: US 60/272,190
  11 <151> PRIOR FILING DATE: 2001-02-28
  13 <150> PRIOR APPLICATION NUMBER: US 60/274,258
  14 <151> PRIOR FILING DATE: 2001-03-07
  16 <160> NUMBER OF SEQ ID NOS: 98
  18 <170> SOFTWARE: PatentIn version 3.0
  20 <210> SEQ ID NO: 1
  21 <211> LENGTH: 1839
  22 <212> TYPE: DNA
  23 <213> ORGANISM: homo sapiens
  25 <220> FEATURE:
  26 <221> NAME/KEY: CDS
  27 <222> LOCATION: (5)..(1057)
  29 <400> SEQUENCE: 1
  30 acaa atg acc ggg agc cat gac gtc atc ggg ggc gca gga aag cag gtg       49
  31      Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val
  32       1               5               10                  15
  34 ctc tgc tgc ttt tgc aag cag aga aat aag agt ttg ggc acc tac cca       97
  35 Leu Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro
  36                  20                  25                  30
  38 ggg gtc cca ggg aat gcc ctg tgg ctc ctg acc tcc ccc gcc tgt aat      145
  39 Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn
  40               35                  40                  45
  42 gct ctg agc act tca gca gta atg cat gga aga gat aag ggg tct gtg      193
  43 Ala Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val
  44          50                  55                  60
  46 acc cat gga act gtc caa gtc ctc tct gac acc cgc ttc ttt tcc tgc      241
  47 Thr His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys
  48      65                  70                  75
  50 cgt gaa gga cta ctt cca gca acc cag tct cct gcc atg tcc gac ccc      289
  51 Arg Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro
  52 80                  85                  90                  95
  54 atc acg ctg aac gtc ggg ggg aag ctc tat aca acc tca ctg gcg acc      337
  55 Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr
  56                  100                 105                 110
  58 ctg acc agc ttc cct gac tcc atg cta ggc gcc atg ttc agc ggg aag      385
  59 Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys
```

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60              115                 120                 125
62 atg ccc acc aag agg gac agc cag ggc aac tgc ttc att gac cgt gac   433
63 Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp
64       130                 135                 140
66 ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt   481
67 Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu
68       145                 150                 155
70 gac ctg cct gag gac ttc cag gag atg ggg ctg ctc cgc agg gag gcc   529
71 Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala
72 160                 165                 170                 175
74 gac ttc tac cag gtg cag ccc ctg att gag gcc ctg cag gag aag gaa   577
75 Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu
76                 180                 185                 190
78 gtg gag ctc tcc aag gcc gag aag aat gcc atg ctc aac atc aca ctg   625
79 Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu
80       195                 200                 205
82 aac cag cgt gtg cag acg gtc cac ttc act gtg cgc gag gca ccc cag   673
83 Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln
84       210                 215                 220
86 atc tac agc ctc tcc tct tcc agc atg gag gtc ttc aac gcc aac atc   721
87 Ile Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile
88       225                 230                 235
90 ttc agc acc tcc tgc ctc ttc ctc aag ctc ctt ggc tct aag ctc ttc   769
91 Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe
92 240                 245                 250                 255
94 tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac   817
95 Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp
96                 260                 265                 270
98 ccc aac cac ctg act ctg gac tgg gtg gcc aat gtg gag ggc ctg cca   865
99 Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro
100            275                 280                 285
102 gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc   913
103 Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro
104            290                 295                 300
106 gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg   961
107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu
108       305                 310                 315
110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat  1009
111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His
112 320                 325                 330                 335
114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg  1057
115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
116            340                 345                 350
118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc  1117
120 ttggagggca tctcgccagt ggtgcgaggc agggggactat actaatctgt attaattgtg  1177
122 tagcaggact tgattccccc catgatgaag tccacctttt ggaatccagt gtcctctgaa  1237
124 cagaaccacc ttttttcttg ccattttgag ctgcagacag gcggtttatt atgacaagtg  1297
126 aagagtcagc tgatgtgtac taaaggaggc cataggagga ttttccagcc aggacaaaag  1357
128 agcagcagtt ttctcctggg ctccatctct ctgtaccgct agccagtgcc gcatttatcc  1417
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          Input Set : A:\EP.txt
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```
130 atctgtaaga aggccctggt ggagaggatg ggatgagaac aagaggctac ctccagttaa   1477
132 ccaggacata aagtccccag cggttcctgt cacacctgct cctccctccc cagggtgcat   1537
134 ccatgatcgt ggatgtttgc ccaggggtga ccatgtttgg ctggcttgga atgctgtgca   1597
136 ttctcagagc tctgttagtg tcccctcttg ggggtcagag atgaggtgtg gcagggtcta   1657
138 gaggaatgag tgtccaggca gagttcagaa ggtaggaatg tccctcttga tagggctgaa   1717
140 tcaagggatt cctggcttta gaaagggtct gctatctttg caaaaatgtg caagtatctg   1777
142 tagccagtgt aatgaaatca cttccaaatc caaaaaaaaa aaaaaaaaa aaaaaaaaa   1837
144 aa                                                                  1839
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 351
149 <212> TYPE: PRT
150 <213> ORGANISM: homo sapiens
152 <400> SEQUENCE: 2
154 Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val Leu
155 1               5                   10                  15
158 Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly
159             20                  25                  30
162 Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn Ala
163         35                  40                  45
166 Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val Thr
167     50                  55                  60
170 His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys Arg
171 65                  70                  75                  80
174 Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro Ile
175                 85                  90                  95
178 Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr Leu
179                 100                 105                 110
182 Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys Met
183         115                 120                 125
186 Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp Gly
187     130                 135                 140
190 Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu Asp
191 145                 150                 155                 160
194 Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala Asp
195                 165                 170                 175
198 Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu Val
199                 180                 185                 190
202 Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu Asn
203         195                 200                 205
206 Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile
207     210                 215                 220
210 Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile Phe
211 225                 230                 235                 240
214 Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe Tyr
215                 245                 250                 255
218 Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp Pro
219             260                 265                 270
222 Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro Glu
223         275                 280                 285
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PATENT APPLICATION: US/10/086,156   TIME: 16:22:30

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226 Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro Ala
227     290             295             300
230 Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu Lys
231 305             310             315                 320
234 Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His Ala
235                 325             330                 335
238 Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
239             340             345             350
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 237
244 <212> TYPE: PRT
245 <213> ORGANISM: homo sapiens
247 <400> SEQUENCE: 3
249 Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
250 1           5               10              15
252 Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
253         20              25              30
255 Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
256         35              40              45
258 Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
259     50              55              60
261 Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
262 65              70              75              80
264 Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
265             85              90              95
267 Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
268             100             105             110
270 Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
271         115             120             125
273 Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
274     130             135             140
276 Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
277 145             150             155             160
279 Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
280             165             170             175
282 Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
283             180             185             190
285 His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
286         195             200             205
288 Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
289     210             215             220
291 Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
292 225             230             235
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 256
296 <212> TYPE: PRT
297 <213> ORGANISM: homo sapiens
299 <220> FEATURE:
300. <221> NAME/KEY: UNSURE
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RAW SEQUENCE LISTING   DATE: 03/19/2002
PATENT APPLICATION: US/10/086,156   TIME: 16:22:30

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\03192002\J086156.raw**

```
   301 <222> LOCATION: (15)..(15)
   302 <223> OTHER INFORMATION: wherein "X" is equal to any amino acid.
   305 <400> SEQUENCE: 4
W-->307 Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn
   308 1               5                   10                  15
   310 Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
   311             20                  25                  30
   313 His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
   314         35                  40                  45
   316 Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
   317     50                  55                  60
   319 Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
   320 65                  70                  75                  80
   322 Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
   323             85                  90                  95
   325 Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
   326             100                 105                 110
   328 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
   329         115                 120                 125
   331 Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
   332     130                 135                 140
   334 Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
   335 145                 150                 155                 160
   337 Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
   338             165                 170                 175
   340 Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
   341             180                 185                 190
   343 Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
   344         195                 200                 205
   346 Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
   347     210                 215                 220
   349 Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
   350 225                 230                 235                 240
   352 Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
   353             245                 250                 255
   355 <210> SEQ ID NO: 5
   356 <211> LENGTH: 234
   357 <212> TYPE: PRT
   358 <213> ORGANISM: homo sapiens
   360 <400> SEQUENCE: 5
   362 Met Pro His Arg Lys Glu Arg Pro Ser Gly Ser Ser Leu His Thr His
   363 1               5                   10                  15
   365 Gly Ser Thr Gly Thr Ala Glu Gly Gly Asn Met Ser Arg Leu Ser Leu
   366             20                  25                  30
   368 Thr Arg Ser Pro Val Ser Pro Leu Ala Ala Gln Gly Ile Pro Leu Pro
   369         35                  40                  45
   371 Ala Gln Leu Thr Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Ser
   372     50                  55                  60
   374 His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Asp Ser
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VERIFICATION SUMMARY   DATE: 03/19/2002
PATENT APPLICATION: US/10/086,156   TIME: 16:22:31

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\03192002\J086156.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8